

=&gt; D BIB ABS L15 1

L15 ANSWER 1 OF 8 HCAPLUS COPYRIGHT 2001 ACS

AN 2000:876805 HCAPLUS

DN 134:39450

TI A high molecular weight bacteriocin of *Serratia plymuthica* with subunits showing similarity to bacteriophage structural proteins

IN Thonart, Philippe; Jabrane, Abdelhamid; Destain, Jacqueline; Pierrard, Annick; Drion, Raphael; Jacques, Philippe

PA Agrostar, Belg.

SO Eur. Pat. Appl., 22 pp.

CODEN: EPXXDW

DT Patent

LA French

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 1059355	A1	20001213	EP 1999-870124	19990611
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
WO 2000077212	A1	20001221	WO 2000-BE62	20000609
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FR, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRAI EP 1999-870124 19990611

AB A high mol. wt. bacteriocin is described from *Serratia plymuthica*. The protein is a heterodimer with the major subunit that has an N-terminal sequence similar to the tail tube protein of phage 186 and a minor subunit with an N-terminal similar to the FI protein of phage P2. The bacteriocin has a spectrum of action typical of a high mol. wt. bacteriocin.

RE.CNT 6

RE

(1) Microlife Technics; EP 0182106 A 1986 HCAPLUS

(2) Nakayama, K; MOLECULAR MICROBIOLOGY 1999, V31(2), P399 HCAPLUS

(3) Shinomiya, T; JOURNAL OF VIROLOGY 1979, V32, P958 MEDLINE

(4) Temple; VIROLOGY 1991, V181(1), P353 HCAPLUS

(6) Xue; VIROLOGY 1995, V212(1), P218 HCAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

=&gt; D BIB ABS L15 2

L15 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2001 ACS

AN 1999:796054 HCAPLUS

DN 132:46951

TI A method of identifying ligands to RNA polymerase .sigma.-70 subunit

IN Balganes, Tanjore; Ramachandran, Vasanthi; Sharma, Umender

PA Astra AB, Swed.

SO PCT Int. Appl., 37 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9964866	A1	19991216	WO 1999-SE979	19990607
W: AL, AM, AT, AU, <u>AZ</u> , BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRAI IN 1998-MA1239		19980609		
SE 1998-2573		19980717		
AB A method of identifying a ligand of a bacterial .sigma.70 subunit comprises contacting the .sigma.70 subunit or a portion thereof comprising the anti-.sigma. binding region, with a test compd. and a fusion protein of an anti-.sigma.70 factor (AsiA) of bacteriophage T4, and detg. whether the test compd. binds competitively interferes with binding of AsiA to the .sigma.70 subunit or portion thereof. A competitive ELISA for quantitation of AsiA-.sigma.70 interaction is described. With use of the .sigma.70 subunit from Escherichia coli, Salmonella typhimurium, or Mycobacterium tuberculosis (sigA or sigB genes), the method provides an assay for antibacterial ligands.				
RE.CNT 3				
RE				
(1) ASTRA Aktiebolag; WO 9638478 A1 1996 HCAPLUS				
(2) Orsini, G; J Bacteriol 1993, V175(1), P85 HCAPLUS				
(3) Research Foundation of State University of New York; WO 9625170 A1 1996 HCAPLUS				

=&gt; D IND 2

L15 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2001 ACS

IC G01N335-69

CC 7-3 (Enzymes)

Section cross-reference(s): 3, 63

ST sigma70 factor inhibition ELISA assay; Mycobacterium sigma70 factor inhibitor screening; RNA polymerase sigma70 inhibitor screening; antisigma factor bacteriophage T4 inhibitor screening

IT Proteins, specific or class

 RL: ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)  
 (AsiA (anti-transcription factor .sigma.-70 inhibitory factor); method of identifying ligands to RNA polymerase .sigma.-70 subunit)

 IT Coliphage T4  
 (anti-.sigma.-70 subunit factor from; method of identifying ligands to RNA polymerase .sigma.-70 subunit)

 IT Immunoassay  
 (enzyme-linked immunosorbent assay, competitive; method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT Antibacterial agents

Drug screening

(method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT Escherichia coli

Mycobacterium tuberculosis

Salmonella typhimurium

(sigma.-70 subunit from; method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT Transcription factors

RL: ARU (Analytical role, unclassified); BPR (Biological process); ANST

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Page 2

(Analytical study); BIOL (Biological study); PROC (Process)  
 (.sigma.-70; method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT 9014-24-8, RNA polymerase 149224-56-6 202608-26-2  
 RL: ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)  
 (method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT 50812-37-8DP, Glutathione S-transferase, fusion protein with anti-.sigma.70 factor from phage T4  
 RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)  
 (method of identifying ligands to RNA polymerase .sigma.-70 subunit)

IT 252656-94-3, 1: PN: WO9964866 SEQID: 4 unclaimed DNA 252656-96-5, 2: PN: WO9964866 SEQID: 5 unclaimed DNA 252656-97-6, 3: PN: WO9964866 SEQID: 6 unclaimed DNA 252657-00-4, 4: PN: WO9964866 SEQID: 7 unclaimed DNA 252657-01-5, 5: PN: WO9964866 SEQID: 8 unclaimed DNA 252657-03-7, 6: PN: WO9964866 SEQID: 3 unclaimed DNA  
 RL: PRP (Properties)  
 (unclaimed nucleotide sequence; method of identifying ligands to RNA polymerase .sigma.-70 subunit)

=&gt; D BIB ABS L15 3

L15 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2001 ACS

AN 1998:709373 HCAPLUS

DN 129:310878

TI Lysozyme-derived peptides and proteins with antimicrobial activity but no muramidase activity, their preparation and their application

IN Duering, Klaus

PA Germany

SO Ger., 8 pp.

CODEN: GWXXAW

DT Patent

LA German

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 19749973	C1	19981022	DE 1997-19749973	19971105
	WO 9924589	A2	19990520	WO 1998-DE3287	19981031
	WO 9924589	A3	19991104		
	W: AU, CA, IL, JP, NZ, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9918679	A1	19990531	AU 1999-18679	19981031
	EP 1029061	A2	20000823	EP 1998-963336	19981031
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI				
PRAI	DE 1997-19749973		19971105		
	WO 1998-DE3287		19981031		
AB	The title peptides/proteins are claimed. They may be prepd. by proteolytic processing of lysozyme, by chem. synthesis, or by use of recombinant organisms. The peptides/proteins may be used in human and veterinary medicine and in agriculture. Thus, it was found that heat-denatured T4 lysozyme was as effective as enzymically active lysozyme in killing of Escherichia coli and Phytophthora nicotianae. An amphipathic helix in the C-terminus (PNRAKRVIFTFT, residues 143-155) displayed antimicrobial activity.				

=&gt; D IND 3

L15 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2001 ACS

IC ICM C07K014-195

ICS A61K038-16

CC 1-5 (Pharmacology)

ST Section cross-reference(s): 5

IT lysozyme fragment antimicrobial

IT Antimicrobial agents

(lysozyme-derived peptides and proteins with antimicrobial activity but no muramidase activity, their prepn. and their application)

IT Protein sequences

(of antimicrobial fragments of lysozyme)

IT 214551-03-8 214551-05-0 214602-93-4 214609-63-9, Lysozyme deriv. (bacteriophage T4)

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(amino acid sequence; lysozyme-derived peptides and proteins with antimicrobial activity but no muramidase activity, their prepn. and their application)

IT 9001-63-2, Lysozyme 214491-09-5 214491-10-8

RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(lysozyme-derived peptides and proteins with antimicrobial activity but no muramidase activity, their prepn. and their application)

IT 214602-92-3

RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(residues 124-164 of lysozyme; lysozyme-derived peptides and proteins with antimicrobial activity but no muramidase activity, their prepn. and their application)

=&gt; D BIB ABS L15 4

L15 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1998:611133 HCAPLUS  
 DN 130:32526  
 TI Bacteriophage T4, a model system for understanding the mechanism of type II topoisomerase inhibitors  
 AU Kreuzer, Kenneth N.  
 CS Department of Microbiology, Duke University Medical Center, Durham, NC, 27710, USA  
 SO Biochim. Biophys. Acta (1998), 1400(1-3), 339-347  
 CODEN: BBACAQ; ISSN: 0006-3002  
 PB Elsevier Science B.V.  
 DT Journal; General Review  
 LA English  
 AB A review with 60 refs. Bacteriophage T4 provides a simple model system for analyzing the mechanism of action of antitumor agents that inhibit DNA topoisomerases. The phage-encoded type II topoisomerase is sensitive to many of the same antitumor agents that inhibit mammalian type II topoisomerase, including m-AMSA, ellipticines, mitoxantrone and epipodophyllotoxins. Results from the T4 model system provided a convincing demonstration that topoisomerase is the physiol. drug target and strong evidence that the drug-induced cleavage complex is important for cytotoxicity. The detailed mol. steps involved in cytotoxicity, and the mechanism of recombinational repair of inhibitor-induced DNA damage, are currently being analyzed using this model system. Studies with the T4 topoisomerase have also provided compelling evidence that topoisomerase inhibitors interact with DNA at the active site of the enzyme, with each class of inhibitor favoring a different subset of cleavage sites based on DNA sequence. Finally, anal. of drug-resistance mutations in the T4 topoisomerase have implicated certain regions of the protein in drug interaction and provided a strong link between the mechanism of action of the antibacterial quinolones, which inhibit DNA gyrase, and the various antitumor agents, which inhibit mammalian type II topoisomerase.

RE.CNT 60  
 RE  
 (1) Barry, J; J Biol Chem 1994, V269, P33049 HCAPLUS  
 (2) Beck, W; DNA Topoisomerases: Topoisomerase-Targeting Drugs 1994, P145 HCAPLUS  
 (3) Berger, J; Nature 1996, V379, P225 HCAPLUS  
 (5) Bernstein, C; Microbiol Rev 1981, V45, P72 HCAPLUS  
 (6) Caldecott, K; Cancer Res 1990, V50, P5778 HCAPLUS  
 ALL CITATIONS AVAILABLE IN THE RE FORMAT

=&gt; D IND 4

L15 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 CC 1-0 (Pharmacology)  
 Section cross-reference(s): 3  
 ST antibacterial DNA gyrase anticancer resistance bacteriophageT4 model topoisomeraseII review  
 IT Antibacterial agents  
 Antitumor agents  
 Coliphage T4  
 Drug resistance  
 (bacteriophage T4, a model system for understanding the mechanism of type II topoisomerase inhibitors)  
 IT DNA gyrases  
 RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
 (bacteriophage T4, a model system for understanding the mechanism of type II topoisomerase inhibitors)  
 IT 142805-56-9D, Topoisomerase II, inhibitors  
 RL: ADV (Adverse effect, including toxicity); BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
 (bacteriophage T4, a model system for understanding the mechanism of type II topoisomerase inhibitors)

=&gt; D BIB ABS L15 5

L15 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1997:542514 HCAPLUS  
 DN 127:186628  
 TI Bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment  
 IN Mardh, Sven  
 PA Mardh, Sven, Swed.  
 SO PCT Int. Appl., 34 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9729185	A1	19970814	WO 1997-SE172	19970205
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	SE 9600434	A	19970807	SE 1996-434	19960206
	SE 506771	C2	19980209		
	CA 2244792	AA	19970814	CA 1997-2244792	19970205
	AU 9716817	A1	19970828	AU 1997-16817	19970205
	AU 712767	B2	19991118		
	EP 889955	A1	19990113	EP 1997-902815	19970205
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	CN 1210558	A	19990310	CN 1997-192116	19970205
	JP 2000505648	T2	20000516	JP 1997-528446	19970205
	NO 9803456	A	19981006	NO 1998-3456	19980727
PRAI	SE 1996-434		19960206		
AB	WO 1997-SE172		19970205		
	The present invention relates to bacteriophages for use in the treatment or prophylaxis of bacterial infections, esp. mucosal bacterial infections such as Helicobacter pylori infections. In particular, it relates to modified filamentous bacteriophages, e.g., M13 phages, for such use, which bacteriophages present at its surface a recombinant protein comprising: (i) a first component derived from a bacteriophage surface protein; and (ii) a second component comprising variable region sequences of an antibody to provide a bacterial antigen binding site, said second component rendering said bacteriophage capable of binding to and thereby inhibiting growth of bacterial cells involved in the etiol. of said infection.				

=&gt; D IND 5

L15 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 IC ICM C12N007-01  
 ICS A61K039-40; C07K016-12; C07K019-00  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 1, 10, 15  
 ST bacteriophage recombinant protein fusion antibody bactericide; surface protein fusion antibody bacteriophage bactericide; bacteria infection recombinant bacteriophage antibody immunotherapy; mucosa bacteria infection bacteriophage antibody immunotherapy  
 IT Hybridomas  
 (2H6; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)  
 IT Hybridomas  
 (5D8; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)  
 IT Hybridomas  
 (5F8; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)

- IT Coliphage M13  
(B8; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Proteins (specific proteins and subclasses)  
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(SU (surface), fusion products, with anti-bacterial-antigen antibody variable domain; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Antibodies  
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(ScFv, fusion products with bacteriophage surface protein; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Antibodies  
Monoclonal antibodies  
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(anti-bacterial-, variable domain, fusion products with bacteriophage surface protein; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Antigens  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(bacterial; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Pilus  
(bacteriophage adsorption to bacterial; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Antibacterial agents  
Bacterial infection  
Filamentous bacteriophage  
Immunotherapy  
(bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Mucous membrane  
(disease; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Proteins (specific proteins and subclasses)  
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)  
(g3p, fusion products, with anti-bacterial-antigen antibody variable domain; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Helicobacter pylori  
(infection; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)
- IT Diseases (animal)  
(mucous membrane; bacteriophages presenting recombinant surface protein fusion products with bacteria antigen-binding antibody for use in bacterial infection treatment)

=&gt; D BIB ABS L15 6

L15 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1996:723060 HCAPLUS  
 DN 126:43276  
 TI A foreign lysozyme as a new tool for antibacterial resistance breeding in transgenic plants  
 AU Duering, Klaus; Porsch, Petra  
 CS Federal Centre Breeding Research Cultivated Plants, Institute Breeding Methods Vegetables, Quedlinburg, D-06484, Germany  
 SO Zuechtungsforschung (1995), 1(2, 75 Years of Phytopathological and Resistance Research at Aschersleben), 219-221  
 CODEN: ZUECF6; ISSN: 0948-5538  
 PB Bundesanstalt fuer Zuechtungsforschung an Kulturpflanzen  
 DT Journal  
 LA English  
 AB Antibacterial resistance is extremely difficult to achieve in potato by conventional breeding methods, as no suitable resistance traits are available in current breeding material. Gene technol. might be a new means of approach to reduce susceptibility to such bacterial pathogens as *Erwinia carotovora*. The introduction of bacteriophage T4 lysozyme into the intercellular spaces of transgenic potato plants might enable an early interaction of the enzyme with invading bacteria, as T4 lysozyme has been shown to possess bacteriolytic activity against several bacteria including *E. carotovora* and *Pseudomonas solanacearum*. In this work, a chimeric fusion gene contg. the barley .alpha.-amylase signal peptide and the bacteriophage T4 lysozyme coding sequence under the control of the CaMV 35S promoter has been cloned into two different vectors. They were used for Agrobacterium-mediated transformation of the tetraploid potato genotype Z2. The protein was successfully expressed, and visualized in intracellular spaces and cell walls.

=&gt; D IND 6

L15 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 7, 10  
 ST T4 lysozyme expression potato  
 IT Cell wall (plant)  
 Coliphage T4  
 Genetic engineering  
 Potato  
 (foreign lysozyme as a new tool for antibacterial resistance breeding in transgenic plants)  
 IT 9001-63-2, Lysozyme  
 RL: BOC (Biological occurrence); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); OCCU (Occurrence)  
 (T4; foreign lysozyme as a new tool for antibacterial resistance breeding in transgenic plants)

=&gt; D BIB ABS L15 7

L15 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1996:474521 HCAPLUS  
 DN 125:186903  
 TI Modified *Listeria* bacteriophage lysin genes (ply) allow efficient overexpression and one-step purification of biochemically active fusion proteins  
 AU Loessner, Martin J.; Schneider, Anette; Scherer, Siegfried  
 CS Inst. Mikrobiol., Tech. Univ. Muenchen, Greising, D-85350, Germany  
 SO Appl. Environ. Microbiol. (1996), 62(8), 3057-3060  
 CODEN: AEMIDF; ISSN: 0099-2240  
 DT Journal  
 LA English  
 AB *Listeria* bacteriophage lytic enzymes are useful for in vitro applications such as rapid, gentle cell disruption, and they provide new approaches as selective antimicrobial agents for destruction of *Listeria monocytogenes* in contaminated foods. We describe here the amino-terminal modification of three cloned *Listeria* phage lysin genes (ply), resulting in fusion proteins with a 12-amino-acid leader contg. six consecutive histidine residues. The recombinant enzymes retain their native specific activity and can be efficiently overproduced in *Escherichia coli*. By one-step metal chelate affinity chromatog., active lysins could be purified to more than 90% homogeneity.

=&gt; D IND 7

L15 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 16, 17  
 ST *Listeria* bacteriophage lysin modification overprodn purifn; gene ply lysin modification cloning phage  
 IT Virus, bacterial  
 (A118; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT Virus, bacterial  
 (A500; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT Virus, bacterial  
 (A511; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT *Escherichia coli*  
 (expression in; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT *Listeria*  
 (modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT Gene, microbial  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)  
 (ply118; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT Gene, microbial  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)  
 (ply500; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT Gene, microbial  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)  
 (ply511; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT 180616-77-7P 180616-78-8P 180616-79-9P  
 RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)  
 (amino acid sequence; modified *Listeria* bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
 IT 9013-25-6P, N-Acetyl-muramoyl-L-alanine amidase 170347-47-4P,

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L-Alanyl-D-glutamate peptidase  
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)  
(modified Listeria bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)  
IT 166355-50-6, Genbank x85008 166355-51-7, Genbank x85009 166355-52-8, Genbank x85010  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(modified Listeria bacteriophage lysin ply genes allow efficient overexpression and one-step purifn. of biochem. active fusion proteins)

=&gt; D BIB ABS L15 8

L15 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 AN 1990:192764 HCAPLUS  
 DN 112:192764  
 TI envM genes of Salmonella typhimurium and Escherichia coli  
 AU Turnowsky, Friederike; Fuchs, Karoline; Jeschek, Claudia; Hoegenauer, Gregor  
 CS Inst. Mikrobiol., Univ. Graz, Graz, A-8010, Austria  
 SO J. Bacteriol. (1989), 171(12), 6555-65  
 CODEN: JOBAAY; ISSN: 0021-9193  
 DT Journal  
 LA English  
 AB Conjugation and bacteriophage P1 transduction expts. in E. coli showed that resistance to the antibacterial compd. diazaborine is caused by an allelic form of the envM gene. The envM gene from S. typhimurium was cloned and sequenced. It codes for a 27,765-dalton protein. The plasmids carrying this DNA complemented a conditionally lethal envM mutant of E. coli. Recombinant plasmids contg. gene envM from a diazaborine-resistant S. typhimurium strain conferred the drug resistance phenotype to susceptible E. coli cells. A guanine-to-adenine exchange in the envM gene changing a Gly codon to a Ser codon was shown to be responsible for the resistance character. Upstream of envM a small gene coding for a 10,445-dalton protein was identified. Incubating a temp.-sensitive E. coli envM mutant at the nonpermissive temp. caused effects on the cells similar to those caused by treatment with diazaborine, i.e., inhibition of fatty acid, phospholipid, and lipopolysaccharide biosynthesis, induction of a 28,000-dalton inner membrane protein, and change in the ratio of the porins OmpC and OmpF.

=&gt; D IND 8

L15 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2001 ACS  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 6  
 ST Salmonella gene envM sequence; mutation Salmonella gene envM diazaborine resistance; Escherichia gene envM diazaborine  
 IT Salmonella typhimurium  
 (gene envM of, diazaborine-resistance mutation in and sequence and physiol. role of)  
 IT Escherichia coli  
 (gene envM of, mapping of, Salmonella typhimurium gene envM conferring diazaborine resistance in relation to)  
 IT Mutation  
 (in gene envM of Salmonella typhimurium, conferring diazaborine resistance)  
 IT Protein sequences  
 (of 10,400-mol.-wt. protein encoded by ORF-1, of Salmonella typhimurium, complete)  
 IT Gene and Genetic element, microbial  
 RL: BIOL (Biological study)  
 (of 10,400-mol.-wt. protein of Salmonella typhimurium, nucleotide and encoded peptide sequences of)  
 IT Protein sequences  
 (of gene envM protein, of Salmonella typhimurium, complete)  
 IT Deoxyribonucleic acid sequences  
 (10,400-mol.-wt. protein ORF 1-specifying, of Salmonella typhimurium, complete)  
 IT Proteins, specific or class  
 RL: PRP (Properties)  
 (28,000-mol.-wt., diazaborine induction of, in Escherichia coli inner membrane, gene envM in relation to)  
 IT Proteins, specific or class  
 RL: BIOL (Biological study)  
 (ORF 1, 10,400-mol.-wt., of Salmonella typhimurium, amino acid sequence of)  
 IT Proteins, specific or class  
 RL: BIOL (Biological study)  
 (gene envM, of Salmonella typhimurium, amino acid sequence of and diazaborine-resistance mutation in)  
 IT Deoxyribonucleic acid sequences  
 (gene envM protein-specifying, of Salmonella typhimurium, complete)

- IT Porins  
RL: BIOL (Biological study)  
(gene ompF, in Escherichia coli, gene envM effect on)
- IT Porins  
RL: BIOL (Biological study)  
(gene ompC, in Escherichia coli, gene envM effect on)
- IT Gene and Genetic element, microbial  
RL: BIOL (Biological study)  
(envM, of Salmonella typhimurium, diazaborine-resistance mutation in  
and sequence and physiol. role of)
- IT 126729-34-8, Protein (Salmonella typhimurium clone pFT105 10.4-kilodalton  
reduced) 126731-07-5, Protein (Salmonella typhimurium clone pFT501 gene  
envM reduced) 126731-08-6, Protein (Salmonella typhimurium clone pKF403  
gene envM reduced)  
RL: PRP (Properties)  
(amino acid sequence of)
- IT 126730-36-7, Deoxyribonucleic acid (Salmonella typhimurium clone pFT501  
gene envM) 126730-37-8, Deoxyribonucleic acid (Salmonella typhimurium  
clone pFT501 10.4-kilodalton protein gene) 126730-38-9, Deoxyribonucleic  
acid (Salmonella typhimurium clone pKF403 gene envM)  
RL: PRP (Properties); BIOL (Biological study)  
(nucleotide sequence of)
- IT 67398-03-2  
RL: PRP (Properties)  
(Escherichia coli and Salmonella typhimurium resistance to, gene envM  
mutation in)

=&gt; D BIB ABS L45 1

L45 ANSWER 1 OF 4 MEDLINE  
 AN 1998422370 MEDLINE  
 DN 98422370  
 TI Bacteriophage T4, a model system for understanding the mechanism of type II topoisomerase inhibitors.  
 AU Kreuzer K N  
 CS Department of Microbiology, Duke University Medical Center, Durham, NC 27710, USA.. kenneth.kreuzer@duke.edu  
 NC CA60836 (NCI)  
 SO BIOCHIMICA ET BIOPHYSICA ACTA, (1998 Oct 1) 1400 (1-3) 339-47. Ref: 60  
 Journal code: A0W. ISSN: 0006-3002.  
 CY Netherlands  
 DT Journal; Article; (JOURNAL ARTICLE)  
 General Review; (REVIEW)  
 (REVIEW, TUTORIAL)  
 LA English  
 FS Priority Journals; Cancer Journals  
 EM 199902  
 EW 19990204  
 AB Bacteriophage T4 provides a simple model system for analyzing the mechanism of action of antitumor agents that inhibit DNA topoisomerases. The phage-encoded type II topoisomerase is sensitive to many of the same antitumor agents that inhibit mammalian type II topoisomerase, including m-AMSA, ellipticines, mitoxantrone and epipodophyllotoxins. Results from the T4 model system provided a convincing demonstration that topoisomerase is the physiological drug target and strong evidence that the drug-induced cleavage complex is important for cytotoxicity. The detailed molecular steps involved in cytotoxicity, and the mechanism of recombinational repair of inhibitor-induced DNA damage, are currently being analyzed using this model system. Studies with the T4 topoisomerase have also provided compelling evidence that topoisomerase inhibitors interact with DNA at the active site of the enzyme, with each class of inhibitor favoring a different subset of cleavage sites based on DNA sequence. Finally, analysis of drug-resistance mutations in the T4 topoisomerase have implicated certain regions of the protein in drug interaction and provided a strong link between the mechanism of action of the antibacterial quinolones, which inhibit DNA gyrase, and the various antitumor agents, which inhibit mammalian type II topoisomerase.

O

=&gt; D BIB ABS L45 2

L45 ANSWER 2 OF 4 MEDLINE

AN 91056100 MEDLINE

DN 91056100

TI Evidence for a common mechanism of action for antitumor and antibacterial agents that inhibit type II DNA topoisomerases.

AU Huff A C; Kreuzer K N

CS Department of Microbiology and Immunology, Duke University Medical Center, Durham, North Carolina 27710.

NC 5T32CA09111-13 (NCI)

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Nov 25) 265 (33) 20496-505.

~~Journal code: HIV; ISSN: 0021-9258.~~

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals; Cancer Journals

EM 199103

AB Numerous antitumor and antibacterial agents inhibit type II DNA topoisomerases, yielding, in each case, a complex of enzyme covalently bound to cleaved DNA. We are investigating the mechanism of inhibitor action by using the type II DNA topoisomerase of bacteriophage T4 as a model. The T4 topoisomerase is the target of antitumor agent 4'-(9-acridinylamino)-methanesulfon-m-anisidide (m-AMSA) in T4-infected *Escherichia coli*. Two m-AMSA-resistant phage strains were previously isolated, one with a point mutation in topoisomerase subunit gene 39 and the other with a point mutation in topoisomerase subunit gene 52. We report here that the wild-type T4 topoisomerase is inhibited by six additional antitumor agents that also inhibit the mammalian type II topoisomerase: ellipticine, 9-OH-ellipticine, 2-me-9-OH-ellipticinium acetate, mitoxantrone diacetate, teniposide, and etoposide. Further, one or both of the m-AMSA-resistance mutations alters the enzyme sensitivity to each of these agents, conferring either cross-resistance or enhanced sensitivity. Finally, the gene 39 mutation confers on T4 topoisomerase a DNA gyrase-like sensitivity to the gyrase inhibitor oxolinic acid, thus establishing a direct link between the mechanism of action of the anti-bacterial quinolones and that of the antitumor agents. These results strongly suggest that diverse inhibitors of type II topoisomerases share a common binding site and a common mechanism of action, both of which are apparently conserved in the evolution of the type II DNA topoisomerases. Alterations in DNA cleavage site specificity caused by either the inhibitors or the m-AMSA-resistance mutations favor the proposal that the inhibitor binding site is composed of both protein and DNA.

=&gt; D BIB ABS L45 3

L45 ANSWER 3 OF 4 MEDLINE

AN 90078098 MEDLINE

DN 90078098

TI envM genes of Salmonella typhimurium and Escherichia coli.

AU Turnowsky F; Fuchs K; Jeschek C; Hogenauer G

CS Institut für Mikrobiologie, Universität Graz, Austria..

SO JOURNAL OF BACTERIOLOGY, (1989 Dec) 171 (12) 6555-65.

Journal code: HH3. ISSN: 0021-9193.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199003

AB Conjugation and bacteriophage P1 transduction experiments in Escherichia coli showed that resistance to the antibacterial compound diazaborine is caused by an allelic form of the envM gene. The envM gene from Salmonella typhimurium was cloned and sequenced. It codes for a 27,765-dalton protein. The plasmids carrying this DNA complemented a conditionally lethal envM mutant of E. coli. Recombinant plasmids containing gene envM from a diazaborine-resistant S. typhimurium strain conferred the drug resistance phenotype to susceptible E. coli cells. A guanine-to-adenine exchange in the envM gene changing a Gly codon to a Ser codon was shown to be responsible for the resistance character. Upstream of envM a small gene coding for a 10,445-dalton protein was identified. Incubating a temperature-sensitive E. coli envM mutant at the nonpermissive temperature caused effects on the cells similar to those caused by treatment with diazaborine, i.e., inhibition of fatty acid, phospholipid, and lipopolysaccharide biosynthesis, induction of a 28,000-dalton inner membrane protein, and change in the ratio of the porins OmpC and OmpF.

=&gt; D BIB ABS L45 4

L45 ANSWER 4 OF 4 MEDLINE

AN 89384445 MEDLINE

DN 89384445

TI Cloning and DNA sequence analysis of a Lactococcus bacteriophage lysin gene.

AU Shearman C; Underwood H; Jury K; Gasson M

CS Department of Genetics and Microbiology, AFRC Institute of Food Research, Norwich Laboratory, UK..

SO MOLECULAR AND GENERAL GENETICS, (1989 Aug) 218 (2) 214-21.

Journal code: NGP. ISSN: 0026-8925.

CY GERMANY, WEST: Germany, Federal Republic of

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-X16178

EM 198912

AB A gene for the lysin of Lactococcus lactis bacteriophage phi vML3 was cloned using an Escherichia coli/bacteriophage lambda host-vector system. The gene was detected by its expression of antimicrobial activity against L. lactis cells in a bioassay. The cloned fragment was analysed by sub-cloning on to E. coli plasmid vectors and by restriction endonuclease and deletion mapping. Its entire DNA sequence was determined and an open reading frame for the lysin structural gene was identified. The sequenced lysin gene would express a protein of 187 amino acids with a molecular weight of 21,090, which is in good agreement with that of a protein detected after in vitro transcription and translation of DNA encoding the gene. Expression of the lysin gene in E. coli and B. subtilis from an adjacent bacteriophage promoter was readily detected but in L. lactis expression of lysin was found to be lethal. The bacteriophage phi vML3 lysin had sequence homology with protein 15 of B. subtilis bacteriophage PZA. This protein is involved in DNA packaging during bacteriophage maturation rather than in host cell lysis. The cloning and analysis of the phi vML3 lysin gene is of importance in further understanding lactic streptococcal bacteriophages, for the development of positive selection vectors and for biotechnological applications of relevance to the dairy industry.

=&gt; D IND 4

L45 ANSWER 4 OF 4 MEDLINE

CT Check Tags: Support, Non-U.S. Gov't

Amino Acid Sequence

Bacillus subtilis

\*Bacteriophages: GE, genetics

Base Sequence

Chromosome Deletion

\*Cloning, Molecular

DNA, Viral: IP, isolation &amp; purification

Enzymes: BI, biosynthesis

\*Enzymes: GE, genetics

Escherichia coli: GE, genetics

\*Genes, Viral

Leuconostoc

Molecular Sequence Data

Mucoproteins: BI, biosynthesis

\*Mucoproteins: GE, genetics

Restriction Mapping

Sequence Homology, Nucleic Acid

Transformation, Genetic

CN 0 (lysin); 0 (DNA, Viral); 0 (Enzymes); 0 (Mucoproteins)